

SEQUENCE LISTING

<110> KANEKA CORPORATION

<120> PORYPEPTIDE HAVING AMIDASE ACTIVITY AND GENE THEREOF

<130> 5404-161(B040008W001)

<150> PCT/JP2005/000951

<151> 2005-01-26

<150> JP2004-028041

<151> 2004-02-04

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 388

<212> PRT

<213> Arthrobacter sp.

<400> 1

Met Ser Arg Leu Leu Arg Glu His Gly Ile Val Ile Gly Arg Leu Gln
 1 5 10 15

Pro Gly Ser Leu Asn Thr Ile Ala Asp Val Ala Gly Val Arg Val Gly
 20 25 30

His Ser Thr Ile Met Arg Gly Ser Gly Pro Leu Ser Ile Gly His Gly
 35 40 45

Pro Val Arg Thr Gly Val Thr Ala Ile Ile Pro His Glu Gly Asp Ile
 50 55 60

Trp Glu Glu Pro Arg Phe Ala Gly Val Phe Ser Leu Asn Gly Ser Gly
 65 70 75 80

Glu Trp Ser Gly Thr Ser Phe Val Arg Glu Thr Gly Cys Leu Tyr Gly
 85 90 95

Pro Ile Met Thr Thr Asn Ser His Ser Ile Gly Ser Val Arg Asn Ala
 100 105 110

Val Ile Lys Arg Glu Val Ala Arg Arg Gly Ser Leu Glu Arg Leu Pro
 115 120 125

Leu Val Gly Glu Thr Phe Asp Gly Leu Leu Asn Asp Ile Ser Gly Met
 130 135 140

His Val Lys Asp Glu His Val Ala Glu Ala Ile Asp Ser Ala Ser Ala
 145 150 155 160

Asn Val Thr Glu Gly Asn Val Gly Gly Gly Thr Gly Asn Val Cys His
 165 170 175

Gly Phe Lys Gly Gly Ile Gly Ser Ala Ser Arg Val Leu Gln Leu Gly
 180 185 190
 Glu Glu Thr Tyr Thr Leu Gly Val Leu Val Gln Ala Asn His Gly Leu
 195 200 205
 Arg Asp Glu Phe Gln Val Thr Gly Val Pro Val Gly Arg Leu Ile Ser
 210 215 220
 Thr Asp Glu Ile Pro Leu Gly Pro Ser Gly Phe Asp Arg Arg Ser Ser
 225 230 235 240
 Pro His Lys Asn Ser Ile Leu Val Val Val Ala Thr Asp Ala Pro Leu
 245 250 255
 Leu Pro Gly Gln Leu Glu Arg Val Ala His Arg Ser Thr Leu Gly Ile
 260 265 270
 Ala Arg Asn Gly Ala Tyr Ala His Asn Leu Ser Gly Asp Leu Ala Leu
 275 280 285
 Ala Phe Ser Thr Cys Pro Gln Pro Val Ser Gly Tyr Asp Phe Gly Val
 290 295 300
 Asp Thr Ser Pro Gly Thr Ile Arg Ala Leu Pro Asn Ala Ala Thr Ala
 305 310 315 320
 Gly Leu Phe Glu Ala Ala Val Glu Ala Thr Glu Glu Ala Ile Val Ser
 325 330 335
 Ala Leu Val His Ala Asp Thr Cys Thr Gly Ile Asp Asp Arg Val Ala
 340 345 350
 Tyr Gly Leu Glu Ala Ala Arg Leu Ala Arg Ser Ile Ser Glu Tyr Arg
 355 360 365
 Gly Thr Gln Leu Tyr Pro Glu Lys Val Ser Asp Ser His Leu Glu Arg
 370 375 380
 Arg Ser Gln Pro
 385

<210> 2
 <211> 1290
 <212> DNA
 <213> *Arthrobacter* sp.

<220>
 <221> CDS
 <222> (53)..(1219)
 <223> sequence coding for amidase

<400> 2
 agcgcgtcgt ggactgggtg cagaaataca caggcgagcc cgaggacgaa aa atg agc
 Met Ser
 1

cgt	ctg	ctc	cgt	gag	cac	gga	atc	gtc	atc	ggc	cgt	ctc	caa	ccg	ggc	106
Arg	Leu	Leu	Arg	Glu	His	Gly	Ile	Val	Ile	Gly	Arg	Leu	Gln	Pro	Gly	
	5						10					15				
tct	ctg	aac	acc	att	gca	gac	gtc	gca	ggc	gtt	cgc	gta	ggc	cat	tca	154
Ser	Leu	Asn	Thr	Ile	Ala	Asp	Val	Ala	Gly	Val	Arg	Val	Gly	His	Ser	
	20					25					30					
aca	atc	atg	cgc	ggc	tct	ggg	ccc	ctg	tcc	atc	ggc	cat	ggc	cca	gtt	202
Thr	Ile	Met	Arg	Gly	Ser	Gly	Pro	Leu	Ser	Ile	Gly	His	Gly	Pro	Val	
35					40					45					50	
cgc	aca	ggg	gta	aca	gcc	atc	atc	cct	cac	gaa	gga	gac	atc	tgg	gag	250
Arg	Thr	Gly	Val	Thr	Ala	Ile	Ile	Pro	His	Glu	Gly	Asp	Ile	Trp	Glu	
				55				60						65		
gag	cca	cgg	ttc	gcc	ggc	gtc	ttc	tcc	ctg	aat	ggc	agc	ggc	gaa	tgg	298
Glu	Pro	Arg	Phe	Ala	Gly	Val	Phe	Ser	Leu	Asn	Gly	Ser	Gly	Glu	Trp	
			70					75					80			
agc	gga	acc	tcg	ttc	gtc	agg	gag	acc	ggg	tgt	ctt	tat	ggc	cct	atc	346
Ser	Gly	Thr	Ser	Phe	Val	Arg	Glu	Thr	Gly	Cys	Leu	Tyr	Gly	Pro	Ile	
		85					90					95				
atg	acg	acg	aat	tcg	cac	agc	att	gga	tcg	gtc	agg	aac	gcc	gtc	atc	394
Met	Thr	Thr	Asn	Ser	His	Ser	Ile	Gly	Ser	Val	Arg	Asn	Ala	Val	Ile	
	100					105					110					
aag	cgt	gaa	gta	gcc	cgg	cgg	gga	agc	ctg	gag	agg	ctc	cct	ctc	gtg	442
Lys	Arg	Glu	Val	Ala	Arg	Arg	Gly	Ser	Leu	Glu	Arg	Leu	Pro	Leu	Val	
115					120					125					130	
gga	gaa	acc	ttt	gat	ggc	cta	ctc	aat	gac	atc	agc	ggc	atg	cac	gtc	490
Gly	Glu	Thr	Phe	Asp	Gly	Leu	Leu	Asn	Asp	Ile	Ser	Gly	Met	His	Val	
				135					140					145		
aag	gac	gaa	cac	gtg	gcc	gag	gcc	atc	gac	tcc	gcc	tcc	gca	aat	gtt	538
Lys	Asp	Glu	His	Val	Ala	Glu	Ala	Ile	Asp	Ser	Ala	Ser	Ala	Asn	Val	
			150					155					160			
acc	gaa	ggc	aat	gtt	ggc	ggc	ggg	acc	gga	aat	gtt	tgt	cac	ggc	ttc	586
Thr	Glu	Gly	Asn	Val	Gly	Gly	Gly	Thr	Gly	Asn	Val	Cys	His	Gly	Phe	
		165					170					175				
aaa	ggc	ggc	att	gga	agt	gcc	tcg	cgc	gtg	ttg	caa	ttg	ggc	gag	gaa	634
Lys	Gly	Gly	Ile	Gly	Ser	Ala	Ser	Arg	Val	Leu	Gln	Leu	Gly	Glu	Glu	
	180					185					190					
acc	tac	act	ttg	ggg	gtt	ctc	gtc	caa	gcc	aac	cac	ggc	ctt	cgt	gac	682
Thr	Tyr	Thr	Leu	Gly	Val	Leu	Val	Gln	Ala	Asn	His	Gly	Leu	Arg	Asp	
195					200					205					210	
gaa	ttt	cag	gtg	acg	gga	gta	ccc	gtg	gga	agg	ctc	ata	tct	acg	gac	730
Glu	Phe	Gln	Val	Thr	Gly	Val	Pro	Val	Gly	Arg	Leu	Ile	Ser	Thr	Asp	
				215					220					225		

gag atc ccc ttg ggg cct tca ggt ttt gat cga agg tct tca cca cac	778
Glu Ile Pro Leu Gly Pro Ser Gly Phe Asp Arg Arg Ser Ser Pro His	
230 235 240	
aaa aac agt att ctt gtc gtc gtg gca acc gac gcg cct cta cta ccg	826
Lys Asn Ser Ile Leu Val Val Val Ala Thr Asp Ala Pro Leu Leu Pro	
245 250 255	
ggc caa ctg gaa cgc gtt gct cac cgt tct acc cta ggc att gcc cgt	874
Gly Gln Leu Glu Arg Val Ala His Arg Ser Thr Leu Gly Ile Ala Arg	
260 265 270	
aat ggt gcc tac gcg cac aat ctc agc ggc gac ctt gca ctt gcg ttc	922
Asn Gly Ala Tyr Ala His Asn Leu Ser Gly Asp Leu Ala Leu Ala Phe	
275 280 285 290	
tcc acc tgc ccg cag cct gta agc ggt tac gat ttc gga gtg gat aca	970
Ser Thr Cys Pro Gln Pro Val Ser Gly Tyr Asp Phe Gly Val Asp Thr	
295 300 305	
agt cct ggg acc att cgc gcc ctg ccc aac gcc gca acg gct ggc ctc	1018
Ser Pro Gly Thr Ile Arg Ala Leu Pro Asn Ala Ala Thr Ala Gly Leu	
310 315 320	
ttc gag gcg gcc gtt gag gcc act gag gaa gcg att gtt tcc gcg ctt	1066
Phe Glu Ala Ala Val Glu Ala Thr Glu Glu Ala Ile Val Ser Ala Leu	
325 330 335	
gtc cac gcc gac acc tgc acc ggg atc gat gac agg gtt gcc tat ggg	1114
Val His Ala Asp Thr Cys Thr Gly Ile Asp Asp Arg Val Ala Tyr Gly	
340 345 350	
ttg gag gcg gct cga ctt gct cgt tca att tcg gaa tat cga ggc acc	1162
Leu Glu Ala Ala Arg Leu Ala Arg Ser Ile Ser Glu Tyr Arg Gly Thr	
355 360 365 370	
cag ctg tat ccg gag aaa gtg tcg gat tcc cat ctt gaa cga agg agc	1210
Gln Leu Tyr Pro Glu Lys Val Ser Asp Ser His Leu Glu Arg Arg Ser	
375 380 385	
cag ccg tga ccgccgcgca gccaaagccaa gcaccacccc gggcaaaggc	1259
Gln Pro	
cgggaaacgg tccaacctaa cacgcaacga t	1290

<210> 3
 <211> 1167
 <212> DNA
 <213> *Arthrobacter* sp.

 <220>
 <221> CDS
 <222> (1)..(1167)
 <223> sequence coding for amidase

<400> 3																
atg	agc	cgt	ctg	ctc	cgt	gag	cac	gga	atc	gtc	atc	ggt	cgt	ctc	caa	48
Met	Ser	Arg	Leu	Leu	Arg	Glu	His	Gly	Ile	Val	Ile	Gly	Arg	Leu	Gln	
1			5			10			15							
ccg	ggt	tct	ctg	aac	acc	att	gca	gac	gtc	gca	ggc	gtt	cgc	gta	ggc	96
Pro	Gly	Ser	Leu	Asn	Thr	Ile	Ala	Asp	Val	Ala	Gly	Val	Arg	Val	Gly	
20			25			30										
cat	tca	aca	atc	atg	cgc	ggt	tct	ggg	ccc	ctg	tcc	atc	ggc	cat	ggc	144
His	Ser	Thr	Ile	Met	Arg	Gly	Ser	Gly	Pro	Leu	Ser	Ile	Gly	His	Gly	
35			40			45										
cca	gtt	cgc	aca	ggg	gta	aca	gcc	atc	atc	cct	cac	gaa	gga	gac	atc	192
Pro	Val	Arg	Thr	Gly	Val	Thr	Ala	Ile	Ile	Pro	His	Glu	Gly	Asp	Ile	
50			55			60										
tgg	gag	gag	cca	cgg	ttc	gcc	ggc	gtc	ttc	tcc	ctg	aat	ggc	agc	ggt	240
Trp	Glu	Glu	Pro	Arg	Phe	Ala	Gly	Val	Phe	Ser	Leu	Asn	Gly	Ser	Gly	
65			70			75			80							
gaa	tgg	agc	gga	acc	tcg	ttc	gtc	agg	gag	acc	ggg	tgt	ctt	tat	ggc	288
Glu	Trp	Ser	Gly	Thr	Ser	Phe	Val	Arg	Glu	Thr	Gly	Cys	Leu	Tyr	Gly	
85			90			95										
cct	atc	atg	acg	acg	aat	tcg	cac	agc	att	gga	tcg	gtc	agg	aac	gcc	336
Pro	Ile	Met	Thr	Thr	Asn	Ser	His	Ser	Ile	Gly	Ser	Val	Arg	Asn	Ala	
100			105			110										
gtc	atc	aag	cgt	gaa	gta	gcc	cgg	cgg	gga	agc	ctg	gag	agg	ctc	cct	384
Val	Ile	Lys	Arg	Glu	Val	Ala	Arg	Arg	Gly	Ser	Leu	Glu	Arg	Leu	Pro	
115			120			125										
ctc	gtg	gga	gaa	acc	ttt	gat	ggc	cta	ctc	aat	gac	atc	agc	ggc	atg	432
Leu	Val	Gly	Glu	Thr	Phe	Asp	Gly	Leu	Leu	Asn	Asp	Ile	Ser	Gly	Met	
130			135			140										
cac	gtc	aag	gac	gaa	cac	gtg	gcc	gag	gcc	atc	gac	tcc	gcc	tcc	gca	480
His	Val	Lys	Asp	Glu	His	Val	Ala	Glu	Ala	Ile	Asp	Ser	Ala	Ser	Ala	
145			150			155			160							
aat	gtt	acc	gaa	ggc	aat	gtt	ggc	ggt	ggg	acc	gga	aat	gtt	tgt	cac	528
Asn	Val	Thr	Glu	Gly	Asn	Val	Gly	Gly	Gly	Thr	Gly	Asn	Val	Cys	His	
165			170			175										
ggt	ttc	aaa	ggc	ggt	att	gga	agt	gcc	tcg	cgc	gtg	ttg	caa	ttg	ggc	576
Gly	Phe	Lys	Gly	Gly	Ile	Gly	Ser	Ala	Ser	Arg	Val	Leu	Gln	Leu	Gly	
180			185			190										
gag	gaa	acc	tac	act	ttg	ggg	gtt	ctc	gtc	caa	gcc	aac	cac	ggc	ctt	624
Glu	Glu	Thr	Tyr	Thr	Leu	Gly	Val	Leu	Val	Gln	Ala	Asn	His	Gly	Leu	
195			200			205										
cgt	gac	gaa	ttt	cag	gtg	acg	gga	gta	ccc	gtg	gga	agg	ctc	ata	tct	672
Arg	Asp	Glu	Phe	Gln	Val	Thr	Gly	Val	Pro	Val	Gly	Arg	Leu	Ile	Ser	
210			215			220										

acg gac gag atc ccc ttg ggg cct tca ggt ttt gat cga agg tct tca Thr Asp Glu Ile Pro Leu Gly Pro Ser Gly Phe Asp Arg Arg Ser Ser 225 230 235 240	720
cca cac aaa aac agt att ctt gtc gtc gtg gca acc gac gcg cct cta Pro His Lys Asn Ser Ile Leu Val Val Val Ala Thr Asp Ala Pro Leu 245 250 255	768
cta ccg ggc caa ctg gaa cgc gtt gct cac cgt tct acc cta ggc att Leu Pro Gly Gln Leu Glu Arg Val Ala His Arg Ser Thr Leu Gly Ile 260 265 270	816
gcc cgt aat ggt gcc tac gcg cac aat ctc agc ggc gac ctt gca ctt Ala Arg Asn Gly Ala Tyr Ala His Asn Leu Ser Gly Asp Leu Ala Leu 275 280 285	864
gcg ttc tcc acc tgc ccg cag cct gta agc ggt tac gat ttc gga gtg Ala Phe Ser Thr Cys Pro Gln Pro Val Ser Gly Tyr Asp Phe Gly Val 290 295 300	912
gat aca agt cct ggg acc att cgc gcc ctg ccc aac gcc gca acg gct Asp Thr Ser Pro Gly Thr Ile Arg Ala Leu Pro Asn Ala Ala Thr Ala 305 310 315 320	960
ggc ctc ttc gag gcg gcc gtt gag gcc act gag gaa gcg att gtt tcc Gly Leu Phe Glu Ala Ala Val Glu Ala Thr Glu Glu Ala Ile Val Ser 325 330 335	1008
gcg ctt gtc cac gcc gac acc tgc acc ggg atc gat gac agg gtt gcc Ala Leu Val His Ala Asp Thr Cys Thr Gly Ile Asp Asp Arg Val Ala 340 345 350	1056
tat ggg ttg gag gcg gct cga ctt gct cgt tca att tcg gaa tat cga Tyr Gly Leu Glu Ala Ala Arg Leu Ala Arg Ser Ile Ser Glu Tyr Arg 355 360 365	1104
ggc acc cag ctg tat ccg gag aaa gtg tcg gat tcc cat ctt gaa cga Gly Thr Gln Leu Tyr Pro Glu Lys Val Ser Asp Ser His Leu Glu Arg 370 375 380	1152
agg agc cag ccg tga Arg Ser Gln Pro 385	1167

<210> 4
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer-1

<220>
 <221> misc_feature
 <222> (2)..(2)

<223> n represents a, t, g or c

<220>

<221> misc_feature

<222> (11)..(11)

<223> n represents a, t, g or c

<400> 4

gngarcaygg nathgt

16

<210> 5

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer-2

<220>

<221> misc_feature

<222> (6)..(6)

<223> n represents a, t, g or c

<220>

<221> misc_feature

<222> (15)..(15)

<223> n represents a, t, g or c

<400> 5

gtrtangtyt cytcncc

17

<210> 6

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer-3

<400> 6

tgccattcag ggagaagac

19

<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer-4

<400> 7

cacgtcaagg acgaacac

18

<210> 8
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer-5

 <400> 8
 taattaggat ccagcgcgctc gtggactg 28

 <210> 9
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer-6

 <400> 9
 ataaccggag ctcacgcttg cgtgcttaggt t 31

 <210> 10
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer-7

 <400> 10
 tcctgctcat atgagccgctc tgctccgt 28

 <210> 11
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer-8

 <400> 11
 attctatgag ctcacggctg gctccttcg 29